

Supplementary Tables

Supplementary Table 1 Ingredients of Tarhana samples at 21±2°C. (WF, whole wheat flour; EF, einkorn wheat flour; CF, chickpea flour; PF, purple potato flour; C, baker’s yeast; S, Sourdough).

Ingredients	Amount (g/100g flour)
Flour (WF, EF, CF, PF)	100
Water	50
Yoghurt	40
Yeast (S; C)	2
Salt	1
Garlic powder	0,5
Onion powder	0,5

Supplementary Table 2 Some physicochemical characteristics of the flours. Data are expressed as arithmetic means ± standard deviations. The mean values indicated with different letters (a-d) in the same column are significantly different (p<0.05).

Sample	Moisture (%)	Ash (%)	Acidity (%)	pH
Wheat Flour	12.73±0.09 ^a	0.75±0.19 ^d	0.18±0.00 ^d	6.01±0.1 ^d
Einkorn Flour	9.28±0.38 ^c	1.83±0.11 ^c	0.54±0.00 ^a	6.34±0.1 ^a
Chickpea Flour	9.30±0.00 ^c	2.67±0.09 ^b	1.24±0.00 ^c	6.21±0.1 ^c
Purple Potato Flour	10.60±0.03 ^b	3.82±0.04 ^a	0.36±0.00 ^b	6.26±0.1 ^b

Supplementary Table 3 The sensory properties of Tarhana samples. Data are expressed as arithmetic means $\pm$ standard deviations. The different letters (A-D) in the same column indicate a statistically significant difference between all samples ($p < 0.05$). The different letters (a-c) in the same column indicate a statistically significant difference between samples produced using the same yeast ($p < 0.05$). The sensory analyses were conducted on the version of the Tarhana sample soup. WF, whole wheat flour; EF, einkorn wheat flour; CF, chickpea flour; PF, purple potato flour; C, Commercial yeast; S, Sourdough.

Sample Code	Colour	Smell	Flavour/Taste
C-WF	5.18 $\pm$ 1.81D ^b	5.84 $\pm$ 1.59BCD ^a	5.49 $\pm$ 1.72BC ^a
C-EF	5.98 $\pm$ 1.74BCD ^{ab}	5.62 $\pm$ 1.61CD ^a	5.44 $\pm$ 1.58BC ^a
C-CF	6.50 $\pm$ 1.84AB ^a	5.952 $\pm$ 2.4ABCD ^a	5.28 $\pm$ 2.26C ^a
C-PF	6.34 $\pm$ 2.41ABC ^a	6.18 $\pm$ 2.09ABC ^a	5.50 $\pm$ 2.80BC ^a
S-WF	5.24 $\pm$ 2.20CD ^b	6.72 $\pm$ 1.56AB ^a	7.00 $\pm$ 1.52A ^a
S-EF	5.91 $\pm$ 2.13BCD ^b	6.40 $\pm$ 1.77ABC ^a	5.88 $\pm$ 1.85BC ^{bc}
S-CF	7.14 $\pm$ 1.47A ^a	6.94 $\pm$ 1.72A ^a	6.45 $\pm$ 1.79AB ^{ab}
S-PF	5.37 $\pm$ 2.50BCD ^b	5.10 $\pm$ 2.40D ^b	4.90 $\pm$ 2.06C ^c
Min-Max	5.18-7.14	5.10-6.94	4.90-7.00
Samples Code	Consistency	Mouthfeel	General acceptability
C-WF	6.86 $\pm$ 1.30A ^a	5.57 $\pm$ 1.79BC ^a	5.50 $\pm$ 2.07BCD ^a
C-EF	5.20 $\pm$ 1.77C ^b	5.16 $\pm$ 1.54C ^a	5.22 $\pm$ 1.79CD ^a
C-CF	5.62 $\pm$ 1.68C ^b	5.20 $\pm$ 2.33BC ^a	5.55 $\pm$ 2.27BCD ^a
C-PF	6.92 $\pm$ 1.95A ^a	5.26 $\pm$ 2.88BC ^a	5.28 $\pm$ 2.76CD ^a

S-WF	7.43±1.22A ^a	6.90±1.48A ^a	6.94±1.38A ^a
S-EF	5.83±1.74BC ^b	5.80±1.84ABC ^{bc}	5.90±1.86ABC ^b
S-CF	6.66±1.47AB ^{ab}	6.33±1.76AB ^{ab}	6.52±1.68AB ^{ab}
S-PF	4.18±2.22D ^c	4.92±2.23C ^c	4.75±2.01D ^c
Min-Max	4.18-7.43	4.92-6.90	4.75-6.94

Supplementary Table 4 Pairwise adonis to compare groups. False discovery rate (FDR) did not reveal significant differences between the groups.

Comparisons	SumsOfSqs	F.Model	R2	p.value	FDR
EFB_SDF vs Baseline	0.345289	8.547079	0.460832	0.005	0.062857
PPB_SDF vs Baseline	0.708333	9.550177	0.488496	0.003	0.062857
CFB_SDF vs Baseline	0.772377	10.39725	0.509738	0.007	0.062857
WFS_SDF vs Baseline	0.394589	9.218727	0.479674	0.008	0.062857
Baseline vs PPS_SDF	0.663179	22.58587	0.693119	0.008	0.062857
Baseline vs Cellulose_DF	1.299687	38.76525	0.794936	0.006	0.062857
Baseline vs Inulin_DF	1.314739	45.5416	0.819955	0.008	0.062857
Baseline vs CFS_SDF	0.898878	24.54735	0.710542	0.01	0.06875
EFS_SDF vs Baseline	0.215941	3.910034	0.281094	0.013	0.079444
WFB_SDF vs Baseline	0.405516	7.821507	0.43888	0.02	0.11

Supplementary Table 5 Table shows Dunn's Test Results at Phylum Level

Phylum	group1	group2	p	p.adj (FDR)
Bacteroidota	Baseline	Cellulose	0.000561	0.01543
Bacteroidota	Baseline	CFS_L	0.000477	0.01543
Fusobacteriota	Baseline	Inulin	0.000289	0.015882
Campylobacterota	Baseline	Inulin	0.00075	0.020631
Campylobacterota	Baseline	CFS_L	0.00075	0.020631
Actinobacteriota	Cellulose	PPB_L	0.00067	0.036853
Fusobacteriota	Baseline	Cellulose	0.001673	0.04602
Verrucomicrobiota	Baseline	Inulin	0.00086	0.047284

Supplementary Table 6 Table shows Dunn test results at Genus level of baker's yeast samples

Genus	group1	group2	p	p.adj (FDR)
<i>Erysipelatoclostridium</i>	Cellulose	PPB_L	0.000828	0.017389
<i>Erysipelatoclostridium</i>	Cellulose	EFB_L	0.002028	0.021296
<i>Holdemania</i>	Cellulose	EFB_L	0.002347	0.029383
<i>Holdemania</i>	EFB_L	Inulin	0.002798	0.029383
<i>Megamonas</i>	CFB_L	Inulin	0.004671	0.032696
<i>Megamonas</i>	Inulin	PPB_L	0.003973	0.032696
<i>Bifidobacterium</i>	Cellulose	PPB_L	0.001704	0.035783
<i>Haemophilus</i>	Cellulose	EFB_L	0.001704	0.035783
<i>Haemophilus</i>	Cellulose	WFB_L	0.003973	0.041712

<i>Streptococcus</i>	Cellulose	EFB_L	0.002028	0.042593
<i>UBA1819</i>	EFB_L	Inulin	0.002028	0.042593
<i>Parasutterella</i>	Cellulose	PPB_L	0.005479	0.044871
<i>Parasutterella</i>	Inulin	PPB_L	0.00641	0.044871
<i>Streptococcus</i>	Cellulose	WFB_L	0.004671	0.049045
<i>Akkermansia</i>	EFB_L	Inulin	0.004671	0.049045

Supplementary Table 7 Table shows Dunn test results at Genus level of faecal samples fermented with pre-digested tarhana from sourdough fermentation

Genus	group1	group2	p	p.adj (FDR)
<i>Haemophilus</i>	Cellulose	CFS_L	0.000687	0.014429
<i>Erysipelatoclostridium</i>	Cellulose	CFS_L	0.001194	0.014994
<i>Erysipelatoclostridium</i>	Cellulose	PPS_L	0.001428	0.014994
<i>Streptococcus</i>	Cellulose	CFS_L	0.002853	0.019968
<i>Streptococcus</i>	Cellulose	PPS_L	0.001194	0.019968
<i>Streptococcus</i>	Cellulose	WFS_L	0.002028	0.019968
<i>Haemophilus</i>	Cellulose	PPS_L	0.002028	0.019968
<i>Haemophilus</i>	CFS_L	Inulin	0.002853	0.019968
<i>Paludicola</i>	EFS_L	Inulin	0.001635	0.020576
<i>Haemophilus</i>	Cellulose	EFS_L	0.004671	0.024522
<i>Turicibacter</i>	Cellulose	PPS_L	0.001428	0.025287
<i>Terrisporobacter</i>	Cellulose	PPS_L	0.002408	0.025287

<i>Turicibacter</i>	Inulin	PPS_L	0.002408	0.025287
<i>Terrisporobacter</i>	Inulin	PPS_L	0.002408	0.025287
<i>Haemophilus</i>	Inulin	PPS_L	0.007482	0.031425
<i>Lachnospiraceae NK4A136 group</i>	EFS_L	Inulin	0.004671	0.032696
<i>Erysipelatoclostridium</i>	Cellulose	EFS_L	0.008712	0.035418
<i>Erysipelatoclostridium</i>	Cellulose	WFS_L	0.010119	0.035418
<i>UBA1819</i>	Inulin	PPS_L	0.001704	0.035783
<i>Turicibacter</i>	Cellulose	CFS_L	0.005479	0.03835
<i>Lachnospiraceae UCG-004</i>	EFS_L	Inulin	0.005479	0.03903
<i>Terrisporobacter</i>	Cellulose	WFS_L	0.007482	0.039281
<i>Terrisporobacter</i>	Inulin	WFS_L	0.007482	0.039281
<i>Dialister</i>	EFS_L	Inulin	0.00641	0.044871
<i>UCG-003</i>	EFS_L	Inulin	0.00641	0.044871
<i>Turicibacter</i>	CFS_L	Inulin	0.008712	0.045738
<i>Haemophilus</i>	EFS_L	Inulin	0.015631	0.046893
<i>UBA1819</i>	Inulin	WFS_L	0.004671	0.049045
<i>Streptococcus</i>	Cellulose	EFS_L	0.011726	0.049249

Supplementary Table 8 ANCOMBC Results of faecal samples fermented with baker's yeast produced tarhana. Wheat flour baker's yeast tarhana soup used as a reference.

lfc.taxon	lfc.EFB_SDF	se. EFB_SDF	W. EFB_SDF	p_val. EFB_SDF	q_val. EFB_SDF
<i>Candidatus Soleaferrea</i>	0.398571833	0.085987065	4.635253376	3.57E-06	0.000691611
<i>TM7x</i>	-0.142055005	0.032739456	-4.338954317	1.43E-05	0.001388674
<i>Caproiciproducens</i>	-0.590011243	0.149464378	-3.947504077	7.90E-05	0.005106738
<i>Pediococcus</i>	-1.852972067	0.555425872	-3.336128476	0.000849539	0.041202638
lfc.taxon	lfc.CFB_SDF	se.CFB_SDF	W.CFB_SDF	p_val.CFB_SDF	q_val.CFB_SDF
<i>Megamonas</i>	1.162701104	0.304682325	3.816109465	0.000135572	0.013150521
<i>Gordonibacter</i>	1.64266587	0.42885072	3.830390838	0.00012794	0.013150521
<i>Phascolarctobacterium</i>	1.45526617	0.40592679	3.585045886	0.000337019	0.021793892
<i>HT002</i>	2.489811817	0.763209285	3.262292358	0.001105151	0.043608317
<i>Leuconostoc</i>	1.954102283	0.609626665	3.205408152	0.001348711	0.043608317
<i>Coprobacter</i>	2.185151343	0.6762565	3.231246345	0.001232517	0.043608317
lfc.taxon	lfc.PPB_SDF	se.PPB_SDF	W.PPB_SDF	p_val.PPB_SDF	q_val.PPB_SDF
<i>Senegalimassilia</i>	-2.317131625	0.290476849	-7.976992428	1.50E-15	2.91E-13
<i>Rothia</i>	0.880408257	0.138274217	6.367118027	1.93E-10	1.87E-08
<i>Parasutterella</i>	1.827860911	0.354974054	5.149280318	2.61E-07	1.69E-05
<i>Acinetobacter</i>	2.537169589	0.511971992	4.955680447	7.21E-07	3.50E-05
<i>Phascolarctobacterium</i>	1.605837779	0.330394802	4.8603603	1.17E-06	4.55E-05
<i>Candidatus Soleaferrea</i>	0.903483875	0.189980772	4.755659554	1.98E-06	6.40E-05
<i>Gordonibacter</i>	1.588270691	0.375195854	4.233177613	2.30E-05	0.000638571
<i>Bifidobacterium</i>	1.406020546	0.354748938	3.963424252	7.39E-05	0.001791646
<i>Megamonas</i>	1.139370677	0.293324921	3.884329617	0.000102613	0.002211872
<i>Solobacterium</i>	1.554855553	0.52553169	2.958633293	0.003090066	0.059947275

Supplementary Table 9 ANCOMBC Results of faecal samples fermented with sourdough produced tarhana. Wheat flour sourdough tarhana soup used as a reference.

lfc.taxon	lfc.EFS_SDF	se.EFS_SDF	W.EFS_SDF	p_val. EFS_SDF	q_val. EFS_SDF
<i>Catenibacillus</i>	2.94134613	0.41133115	7.150798405	8.63E-13	1.71E-10
lfc.taxon	lfc.CFS_SDF	se.CFS_SDF	W. CFS_SDF	p_val. CFS_SDF	q_val.CFS_SDF
<i>[Eubacterium] eligens group</i>	-0.403405759	0.048611981	-8.298484208	1.05E-16	2.09E-14
<i>Alistipes</i>	-0.948161056	0.121009621	-7.835418791	4.67E-15	4.39E-13
<i>Catenibacillus</i>	2.856068806	0.366584808	7.791017916	6.65E-15	4.39E-13
<i>Paraprevotella</i>	-3.247945395	0.679043018	-4.783121698	1.73E-06	8.54E-05
<i>Acidaminococcus</i>	-1.238252607	0.273039222	-4.535072276	5.76E-06	0.000228032
<i>Senegalimassilia</i>	0.601447916	0.153802091	3.910531475	9.21E-05	0.00255199
<i>Desulfovibrio</i>	-0.415335755	0.106762843	-3.890265014	0.000100135	0.00255199
<i>Olsenella</i>	0.693693895	0.178641925	3.883152826	0.000103111	0.00255199
<i>Hungatella</i>	0.531320466	0.144096403	3.687256978	0.000226684	0.004987057
<i>Fusicatenibacter</i>	-0.405499795	0.111131137	-3.648840509	0.000263427	0.005215846
<i>UCG-003</i>	-0.795836097	0.233529959	-3.407854394	0.000654758	0.011785648
<i>Fournierella</i>	-0.422492416	0.127552944	-3.312290581	0.000925354	0.013087146
<i>Enterorhabdus</i>	0.335059587	0.100557137	3.332031903	0.000862144	0.013087146
<i>Solobacterium</i>	-0.408163076	0.122332464	-3.336506627	0.000848384	0.013087146
<i>[Eubacterium] xylanophilum group</i>	-1.892370518	0.586696271	-3.225468803	0.001257665	0.015819957
<i>Merdibacter</i>	-1.728653503	0.536717328	-3.220789439	0.00127838	0.015819957
<i>[Eubacterium] ventriosum group</i>	-0.452613432	0.141950851	-3.188522132	0.001430021	0.016655534
<i>Clostridium sensu stricto 13</i>	2.447258634	0.778987684	3.141588352	0.001680341	0.018418127
<i>Coprococcus</i>	-0.644941759	0.206264696	-3.126767559	0.001767396	0.018418127
<i>CAG-56</i>	-1.302720224	0.419153104	-3.107981811	0.001883697	0.018648596
<i>Oscillibacter</i>	-0.546434659	0.180476314	-3.027736136	0.002463931	0.022175381
<i>Oscillospira</i>	-0.70701598	0.233476723	-3.028207575	0.00246009	0.022175381

<i>CAG-352</i>	-1.960746998	0.654136618	-2.997457938	0.002722414	0.023436436
<i>Dialister</i>	-0.388931355	0.133521044	-2.912884325	0.003581072	0.029543846
<i>Lachnospiraceae NK4A136 group</i>	-0.685606028	0.243174912	-2.819394577	0.004811433	0.038106552
<i>Agathobacter</i>	-0.303792706	0.109980416	-2.76224365	0.005740562	0.040640716
<i>NK4A214 group</i>	-0.75503877	0.274050355	-2.755109625	0.005867247	0.040640716
<i>Oxalobacter</i>	-0.681962501	0.248958267	-2.739264336	0.006157684	0.040640716
<i>DTU089</i>	-0.462350582	0.166073491	-2.784011938	0.005369106	0.040640716
<i>Sellimonas</i>	-1.260655524	0.460158018	-2.739614384	0.006151131	0.040640716
<i>Roseburia</i>	-0.95084763	0.349209069	-2.722860642	0.006471935	0.041262572
<i>Adlercreutzia</i>	0.538669782	0.198554931	2.712950909	0.006668699	0.041262572
<i>Granulicatella</i>	0.389507485	0.145964478	2.668508745	0.00761888	0.045713277
<i>Colidextribacter</i>	-1.064889461	0.402174483	-2.647829501	0.008101037	0.047176628
lfc.taxon	lfc.PPS SDF	se.PPS SDF	W.PPS SDF	p_val.PPS SDF	q_val.PPS SDF
<i>Catenibacillus</i>	2.86828237	0.42254977	6.788034387	1.14E-11	2.25E-09
<i>Olsenella</i>	1.395308366	0.210909875	6.615661609	3.70E-11	3.66E-09
<i>Solobacterium</i>	-0.453339241	0.092597165	-4.895822036	9.79E-07	6.46E-05
<i>[Eubacterium] eligens group</i>	-0.186572711	0.046928854	-3.975650303	7.02E-05	0.003474266
<i>CHKCI002</i>	0.831416969	0.215516935	3.857780227	0.000114421	0.00453109
<i>Mogibacterium</i>	1.818321385	0.483241086	3.762762393	0.000168047	0.005545546
<i>Prevotella_7</i>	-2.383384343	0.675730416	-3.527123075	0.000420101	0.010502181
<i>Acetanaerobacterium</i>	-1.174060776	0.333116954	-3.524470198	0.000424331	0.010502181
<i>Collinsella</i>	0.835331582	0.267064656	3.127825275	0.001761048	0.034868758
<i>Libanicoccus</i>	0.945152389	0.300233577	3.148056919	0.001643597	0.034868758